

## IN THE CLAIMS

Cancel claims 1-12 and add new claims 13-24, reading as follows:

--13. (New) A method for the multidimensional analysis of a proteome in which the biological material with the proteome to be analyzed is solubilized and the proteins belonging to the proteome are separated, quantitatively determined and identified, comprising the steps of:

subjecting the proteome to a number  $n$  of different separating processes for  $n > 2$  under standardized conditions in such a way that each of the liquid fractions  $m_1$  obtained in a separating step supplies  $m_2$  liquid fractions in a subsequent separating steps, wherein, after  $n$  separating steps, there are  $m_1 * m_2 * \dots m_n = M$  liquid fractions;

identifying said  $m_1 * m_2 * \dots m_n = M$  liquid fractions by  $\tau$  different analysis processes qualitatively and/or quantitatively by identification processes, and determining said liquid ratio quantitatively by known quantification processes; and

after combining the analysis data, obtaining an  $n$ -dimensional image of the proteome which is characterized by identifiers and quantifiers and by the position in the  $n$ -dimensional data space.

14. (New) The method according to claim 13, wherein methods which separate according to the size of the protein and/or methods which separate according to the mass of the protein and/or methods which separate according to the charge of the protein and/or methods which separate according to the hydrophobicity of the protein and/or methods which separate according to the shape of the protein and/or methods which separate according to the affinity of the protein, with respect to specific ligands, also to antibodies are selected as separating methods.

15. (New). The method according to claim 13, wherein methods for determining specific immunological characteristics and/or methods for determining specific catalytic activity and/or methods for determining chemical

modification of the proteins of the proteome are used as identification methods.

16. (New). The method according to claim 13, wherein methods for nonspecific determination of protein concentration with different sensitivities and/or quantitative determination methods for determining specific catalytic activities and/or quantitative immunological methods and/or quantitative binding assays are selected as quantification methods.

17. (New). The method according to claim 13, wherein the identification of individual proteins of the proteome is carried out directly by mass determination of the proteins.

18. (New) The method according to claim 13, wherein the identification of individual proteins is carried out according to protease digestion and mass identification of fragments.

19. (New) The method according to claim 13 wherein, after the separation step, the fractions are assembled in a two-dimensional multiple vessel system, in the manner of and with the layout of microtitration plates.

20. (New). The method according to claim 13 wherein, in the first separating step, the fractions are assembled in a defined grid, preferably in the  $n * 96$  grid of microtitration technology.

21. (New) The method according to claim 13, wherein all identification and quantification steps are carried out in a defined grid, preferably in the  $n * 96$  grid, with adaptable liquid handling technique.

22. (New) The method according to claim 21, wherein all identification steps and quantification steps are carried out with at least four two-dimensionally arranged, simultaneously working pipettor channels.

23. (New). The method according to claim 13, wherein the first

dimension for separation is high-resolution size exclusion, ion exchange or hydrophobicity chromatography, which are known per se, in that the second dimension is carried out by parallel separation and fractionation of the fractions of the first dimension by a principle of separation other than that used for the first dimension, and in that each further separation and fractionation is carried out by parallel separating and fractionating methods with the fractions obtained from the preceding separating and fractionating steps.

24. (New) The method according to claim 13, wherein the analysis data for the n-dimensional image of the protein are assembled in a database.--

10030062-043002